SEQUENCE LISTING

<110> Lassner, Michael
Post-Beittenmiller, Dusty
Savidge, Beth
Weiss, James

<120> Nucleic Acid Sequences Involved in Tocopherol Synthesis

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<140> 09/549,848
<141> 2000-04-14

<150> 60/129,899
<151> 1999-04-15

<150> 60/146,461
<151> 1999-07-30

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35 40 45
Arg Asn Asn Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu
50 55 60

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Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr
            100                 105                 110
Val Leu Ser Ile Leu Ser Val Ser Phe Leu Ala Val Glu Lys Val Ser
        115                 120                 125
Asp Ile Ser Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala
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Ala Leu Met Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp
145                 150                 155                 160
Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly
                165                 170                 175
Glu Tyr Ser Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile
            180                 185                 190
Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp
        195                 200                 205
Ala Leu Phe Val Ser Phe Met Leu Gly Thr Ala Tyr Ser Ile Asn Leu
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Pro Leu Leu Arg Trp Lys Arg Phe Ala Leu Val Ala Ala Met Cys Ile
225                 230                 235                 240
Leu Ala Val Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile
                245                 250                 255
Gln Thr His Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile
            260                 265                 270
Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe
        275                 280                 285
Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser
    290                 295                 300
Phe Ser Val Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr
305                 310                 315                 320
Leu Leu Gln Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser
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Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu
            340                 345                 350
Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys
        355                 360                 365
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<211> 407
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<213> Arabidopsis sp

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35 40 45
Thr Lys Cys Tyr Pro Ser Trp Asn Asp Asn Tyr Gln Val Trp Ser Lys
50 55 60
Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr
65 70 75 80
Arg Leu Ile Cys Gly Met Ser Ser Ser Ser Ser Val Leu Glu Gly Lys
85 90 95
Pro Lys Lys Asp Asp Lys Glu Lys Ser Asp Gly Val Val Val Lys Lys
100 105 110
Ala Ser Trp Ile Asp Leu Tyr Leu Pro Glu Glu Val Arg Gly Tyr Ala
115 120 125
Lys Leu Ala Arg Leu Asp Lys Pro Ile Gly Thr Trp Leu Leu Ala Trp
130 135 140
Pro Cys Met Trp Ser Ile Ala Leu Ala Ala Asp Pro Gly Ser Leu Pro
145 150 155 160
Ser Phe Lys Tyr Met Ala Leu Phe Gly Cys Gly Ala Leu Leu Leu Arg
165 170 175
Gly Ala Gly Cys Thr Ile Asn Asp Leu Leu Asp Gln Asp Ile Asp Thr
180 185 190
Lys Val Asp Arg Thr Lys Leu Arg Pro Ile Ala Ser Gly Leu Leu Thr
195 200 205
Pro Phe Gln Gly Ile Gly Phe Leu Gly Leu Gln Leu Leu Leu Gly Leu
210 215 220
Gly Ile Leu Leu Gln Leu Asn Asn Tyr Ser Arg Val Leu Gly Ala Ser
225 230 235 240
Ser Leu Leu Leu Val Phe Ser Tyr Pro Leu Met Lys Arg Phe Thr Phe
245 250 255
Trp Pro Gln Ala Phe Leu Gly Leu Thr Ile Asn Trp Gly Ala Leu Leu
260 265 270
Gly Trp Thr Ala Val Lys Gly Ser Ile Ala Pro Ser Ile Val Leu Pro
275 280 285
Leu Tyr Leu Ser Gly Val Cys Trp Thr Leu Val Tyr Asp Thr Ile Tyr
290 295 300
Ala His Gln Asp Lys Glu Asp Asp Val Lys Val Gly Val Lys Ser Thr
305 310 315 320
Ala Leu Arg Phe Gly Asp Asn Thr Lys Leu Trp Leu Thr Gly Phe Gly
325 330 335
Thr Ala Ser Ile Gly Phe Leu Ala Leu Ser Gly Phe Ser Ala Asp Leu
340 345 350
Gly Trp Gln Tyr Tyr Ala Ser Leu Ala Ala Ala Ser Gly Gln Leu Gly
355 360 365
Trp Gln Ile Gly Thr Ala Asp Leu Ser Ser Gly Ala Asp Cys Ser Arg
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<211> 1296

<212> DNA
<213> Arabidopsis sp

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<213> Arabidopsis sp

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35 40 45
Ala Lys Leu Gly Ile Thr Gly Val Arg Ser Asp Ala Asn Arg Val Phe
50 55 60
Ala Thr Ala Thr Ala Ala Ala Thr Ala Thr Ala Thr Thr Gly Glu Ile
65 70 75 80
Ser Ser Arg Val Ala Ala Leu Ala Gly Leu Gly His His Tyr Ala Arg
85 90 95
Cys Tyr Trp Glu Leu Ser Lys Ala Lys Leu Ser Met Leu Val Val Ala
100 105 110
Thr Ser Gly Thr Gly Tyr Ile Leu Gly Thr Gly Asn Ala Ala Ile Ser
115 120 125
Phe Pro Gly Leu Cys Tyr Thr Cys Ala Gly Thr Met Met Ile Ala Ala
130 135 140
Ser Ala Asn Ser Leu Asn Gln Ile Phe Glu Ile Ser Asn Asp Ser Lys
145 150 155 160
Met Lys Arg Thr Met Leu Arg Pro Leu Pro Ser Gly Arg Ile Ser Val
165 170 175
Pro His Ala Val Ala Trp Ala Thr Ile Ala Gly Ala Ser Gly Ala Cys
180 185 190
Leu Leu Ala Ser Lys Thr Asn Met Leu Ala Ala Gly Leu Ala Ser Ala
195 200 205
Asn Leu Val Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Gln Leu His
210 215 220
Pro Ile Asn Thr Trp Val Gly Ala Val Val Gly Ala Ile Pro Pro Leu
225 230 235 240
Leu Gly Trp Ala Ala Ala Ser Gly Gln Ile Ser Tyr Asn Ser Met Ile
245 250 255

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Leu Pro Ala Ala Leu Tyr Phe Trp Gln Ile Pro His Phe Met Ala Leu
            260                 265                 270
Ala His Leu Cys Arg Asn Asp Tyr Ala Ala Gly Gly Tyr Lys Met Leu
        275                 280                 285
Ser Leu Phe Asp Pro Ser Gly Lys Arg Ile Ala Ala Val Ala Leu Arg
    290                 295                 300
Asn Cys Phe Tyr Met Ile Pro Leu Gly Phe Ile Ala Tyr Asp Trp Gly
305                 310                 315                 320
Leu Thr Ser Ser Trp Phe Cys Leu Glu Ser Thr Leu Leu Thr Leu Ala
                325                 330                 335
Ile Ala Ala Thr Ala Phe Ser Phe Tyr Arg Asp Arg Thr Met His Lys
            340                 345                 350
Ala Arg Lys Met Phe His Ala Ser Leu Leu Phe Leu Pro Val Phe Met
        355                 360                 365
Ser Gly Leu Leu Leu His Arg Val Ser Asn Asp Asn Gln Gln Gln Leu
    370                 375                 380
Val Glu Glu Ala Gly Leu Thr Asn Ser Val Ser Gly Glu Val Lys Thr
385                 390                 395                 400
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<213> Arabidopsis sp

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<212> DNA
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<400> 9

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        35                  40                  45
Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
    50                  55                  60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65                  70                  75                  80
Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
                85                  90                  95
Val Val Met Gly Asn Lys Val Val Ala Leu Leu Ala Thr Ala Val Glu
            100                 105                 110
His Leu Val Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln
        115                 120                 125
Arg Tyr Ser Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala
    130                 135                 140
Ser Leu Ile Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln
145                 150                 155                 160
Thr Ala Glu Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly
                165                 170                 175
Leu Ala Phe Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser
            180                 185                 190
Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile
        195                 200                 205
Thr Ala Pro Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu
    210                 215                 220
Val Val Asp Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu
225                 230                 235                 240
Glu Tyr Leu Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala
                245                 250                 255
Met Glu His Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu
            260                 265                 270
Thr Asp Asn Glu Asp Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu
        275                 280                 285
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<212> DNA
<213> Arabidopsis sp

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<212> DNA
<213> Arabidopsis sp

<400> 11

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cgcgttccag aagcattgat tggggaatca acagatatag tcacatcaga attacgcgta     180
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<211> 321
<212> PRT
<213> Arabidopsis sp

<400> 12

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Leu Met Ala Thr Ala Leu Asn Val Arg Val Pro Glu Ala Leu Ile Gly
        35                  40                  45
Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
    50                  55                  60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65                  70                  75                  80
Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
                85                  90                  95
Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp Phe Leu Leu
            100                 105                 110
Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr Glu Val Val
        115                 120                 125
Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly Glu Thr Met
    130                 135                 140
Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp Tyr Tyr Met
145                 150                 155                 160
Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys
                165                 170                 175
Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala Val Leu Ala
            180                 185                 190
Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp
        195                 200                 205
Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu
    210                 215                 220
Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu Phe Ala Met
225                 230                 235                 240
Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val Glu Lys Asp
                245                 250                 255
Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys Ser Lys Gly
            260                 265                 270
Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn Leu Ala Ala
        275                 280                 285
Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp Val Lys Arg
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305                 310                 315                 320
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<211> 621

212> DNA
<213> Arabidopsis sp

<400> 13
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taactcttta gcatgtagtc atcaagcttg acatcacaat cgaataaact cgatgcttgc 420
tttatctcac cgcttgcaaa atctttgatc acctgcaaaa agataaatca agattcagac 480
caaatgttct ttgtattgag tagcttcatc taatctcaga aaggaatatt acctgactta 540
tgagcttaat gacttcaagg ttttcgagat ttgtaagtac catgatgctt gagcaacatg 600
aaatccccag ctaatacagc t 621

<210> 14
<211> 741
<212> DNA
<213> Arabidopsis sp

<400> 14
ggtgagtttt gttaatagtt atgagattca tctatttttg tcataaaatt gtttggtttg 60
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gtagcggtgc tagctggaga tttcatgttt gctcaagcgt catggtactt agcaaatctc 180
gagaatcttg aagttattaa gctcatcagt caggtactta gttactctta cattgttttt 240
ctatgaggtt gagctatgaa tctcatttcg ttgaataatg ctgtgcctca aacttttttt 300
catgttttca ggtgatcaaa gactttgcaa gcggagagat aaagcaggcg tccagcttat 360
ttgactgcga caccaagctc gacgagtact tactcaaaag tttctacaag acagcctctt 420
tagtggctgc gagcaccaaa ggagctgcca ttttcagcag agttgagcct gatgtgacag 480
aacaaatgta cgagtttggg aagaatctcg gtctctcttt ccagatagtt gatgatattt 540
tggatttcac tcagtcgaca gagcagctcg ggaagccagc agggagtgat ttggctaaag 600
gtaacttaac agcacctgtg attttcgctc tggagaggga gccaaggcta agagagatca 660
ttgagtcaaa gttctgtgag gcgggttctc tggaagaagc gattgaagcg gtgacaaaag 720
gtgggggat taagagagca c 741

<210> 15
<211> 1087
<212> DNA
<213> Arabidopsis sp

<400> 15
cctcttcagc caatccagag gaagaagaga caacttttta tctttcgtca agagtctccg 60
aaaacgcacg gttttatgct ctctcttctg ccctcacctc acaagacgca gggcacatga 120
ttcaaccaga gggaaaaagc aacgataaca actctgcttt tgatttcaag ctgtatatga 180
tccgcaaagc cgagtctgta aatgcggctc tcgacgtttc cgtaccgctt ctgaaacccc 240
ttacgatcca agaagcggtc aggtactctt tgctagccgg cggaaaacgt gtgaggcctc 300
tgctctgcat tgccgcttgt gagcttgtgg ggggcgacga ggctactgcc atgtcagccg 360
cttgcgcggt cgagatgatc cacacaagct ctctcattca tgacgatctt ccgtgcatgg 420
acaatgccga cctccgtaga ggcaagccca ccaatcacaa ggtatgttgt ttaattatat 480
gaaggctcag agataatgct gaactagtgt tgaaccaatt tttgctcaaa caaggtatat 540
ggagaagaca tggcggtttt ggcaggtgat gcactccttg cattggcgtt tgagcacatg 600
acggttgtgt cgagtgggtt ggtcgctccc gagaagatga ttcgcgccgt ggttgagctg 660
gccagggcca tagggactac agggctagtt gctggacaaa tgatagacct agccagcgaa 720
agactgaatc cagacaaggt tggattggag catctagagt tcatccatct ccacaaaacg 780
gcggcattgt tggaggcagc ggcagtttta ggggttataa tgggaggtgg aacagaggaa 840
gaaatcgaaa agcttagaaa gtatgctagg tgtattggac tactgtttca ggttgttgat 900
gacattctcg acgtaacaaa atctactgag gaattgggta agacagccgg aaaagacgta 960
atggccggaa agctgacgta tccaaggctg ataggtttgg agggatccag ggaagttgca 1020
gagcacctga ggagagaagc agaggaaaag cttaaagggt ttgatccaag tcaggcggcg 1080
cctctgg 1087

<210> 16
<211> 1164
<212> DNA
<213> Arabidopsis sp

<400> 16
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cgagtcggag tcctctctct tcggaattcg gattccgttg agttcactcg ccggcgttct 120
ggtttctcga cgttgatcta cgaatcaccc gggcggagat ttgttgtgcg tgcggcggag 180
actgatactg ataaagttaa atctcagaca cctgacaagg caccagccgg tggttcaagc 240
attaaccagc ttctcggtat caaaggagca tctcaagaaa ctaataaatg gaagattcgt 300
cttcagctta caaaaccagt cacttggcct ccactggttt ggggagtcgt ctgtggtgct 360
gctgcttcag ggaactttca ttggacccca gaggatgttg ctaagtcgat tctttgcatg 420
atgatgtctg gtccttgtct tactggctat acacagacaa tcaacgactg gtatgataga 480
gatatcgacg caattaatga gccatatcgt ccaattccat ctggagcaat atcagagcca 540
gaggttatta cacaagtctg ggtgctatta ttgggaggtc ttggtattgc tggaatatta 600
gatgtgtggg cagggcatac cactcccact gtcttctatc ttgctttggg aggatcattg 660
ctatcttata tatactctgc tccacctctt aagctaaaac aaaatggatg ggttggaaat 720
tttgcacttg gagcaagcta tattagtttg ccatggtggg ctggccaagc attgtttggc 780
actcttacgc cagatgttgt tgttctaaca ctcttgtaca gcatagctgg gttaggaata 840
gccattgtta acgacttcaa aagtgttgaa ggagatagag cattaggact tcagtctctc 900
ccagtagctt ttggcaccga aactgcaaaa tggatatgcg ttggtgctat agacattact 960
cagctttctg ttgccggata tctattagca tctgggaaac cttattatgc gttggcgttg 1020
gttgctttga tcattcctca gattgtgttc cagtttaaat actttctcaa ggaccctgtc 1080
aaatacgacg tcaagtacca ggcaagcgcg cagccattct tggtgctcgg aatatttgta 1140
acggcattag catcgcaaca ctga 1164

<210> 17
<211> 387
<212> PRT
<213> Arabidopsis sp

<400> 17
Met Thr Ser Ile Leu Asn Thr Val Ser Thr Ile His Ser Ser Arg Val
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Thr Ser Val Asp Arg Val Gly Val Leu Ser Leu Arg Asn Ser Asp Ser
            20   25   30
Val Glu Phe Thr Arg Arg Arg Ser Gly Phe Ser Thr Leu Ile Tyr Glu
        35   40   45
Ser Pro Gly Arg Arg Phe Val Val Arg Ala Ala Glu Thr Asp Thr Asp
    50   55   60
Lys Val Lys Ser Gln Thr Pro Asp Lys Ala Pro Ala Gly Gly Ser Ser
65   70   75   80
Ile Asn Gln Leu Leu Gly Ile Lys Gly Ala Ser Gln Glu Thr Asn Lys
                85   90   95
Trp Lys Ile Arg Leu Gln Leu Thr Lys Pro Val Thr Trp Pro Pro Leu
            100   105   110
Val Trp Gly Val Val Cys Gly Ala Ala Ala Ser Gly Asn Phe His Trp
        115   120   125
Thr Pro Glu Asp Val Ala Lys Ser Ile Leu Cys Met Met Met Ser Gly
    130   135   140
Pro Cys Leu Thr Gly Tyr Thr Gln Thr Ile Asn Asp Trp Tyr Asp Arg
145   150   155   160
Asp Ile Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala
                165   170   175
Ile Ser Glu Pro Glu Val Ile Thr Gln Val Trp Val Leu Leu Leu Gly
            180   185   190
Gly Leu Gly Ile Ala Gly Ile Leu Asp Val Trp Ala Gly His Thr Thr
        195   200   205
Pro Thr Val Phe Tyr Leu Ala Leu Gly Gly Ser Leu Leu Ser Tyr Ile
    210   215   220
Tyr Ser Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Val Gly Asn
225   230   235   240
Phe Ala Leu Gly Ala Ser Tyr Ile Ser Leu Pro Trp Trp Ala Gly Gln
                245   250   255
Ala Leu Phe Gly Thr Leu Thr Pro Asp Val Val Val Leu Thr Leu Leu
            260   265   270
Tyr Ser Ile Ala Gly Leu Gly Ile Ala Ile Val Asn Asp Phe Lys Ser
        275   280   285
Val Glu Gly Asp Arg Ala Leu Gly Leu Gln Ser Leu Pro Val Ala Phe
    290   295   300

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Gly Thr Glu Thr Ala Lys Trp Ile Cys Val Gly Ala Ile Asp Ile Thr
305                 310                 315                 320
Gln Leu Ser Val Ala Gly Tyr Leu Leu Ala Ser Gly Lys Pro Tyr Tyr
                325                 330                 335
Ala Leu Ala Leu Val Ala Leu Ile Ile Pro Gln Ile Val Phe Gln Phe
            340                 345                 350
Lys Tyr Phe Leu Lys Asp Pro Val Lys Tyr Asp Val Lys Tyr Gln Ala
        355                 360                 365
Ser Ala Gln Pro Phe Leu Val Leu Gly Ile Phe Val Thr Ala Leu Ala
    370                 375                 380
Ser Gln His
385
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<210> 18
<211> 981
<212> DNA
<213> Arabidopsis sp

<400> 18
atgttgttta gtggttcagc gatcccatta agcagcttct gctctcttcc ggagaaaccc 60
cacactcttc ctatgaaact ctctcccgct gcaatccgat cttcatcctc atctgccccg 120
gggtcgttga acttcgatct gaggacgtat tggacgactc tgatcaccga gatcaaccag 180
aagctggatg aggccatacc ggtcaagcac cctgcgggga tctacgaggc tatgagatac 240
tctgtactcg cacaaggcgc caagcgtgcc cctcctgtga tgtgtgtggc ggcctgcgag 300
ctcttcggtg gcgatcgcct cgccgctttc cccaccgcct gtgccctaga aatggtgcac 360
gcggcttcgt tgatacacga cgacctcccc tgtatggacg acgatcctgt gcgcagagga 420
aagccatcta accacactgt ctacggctct ggcatggcca ttctcgccgg tgacgccctc 480
ttcccactcg ccttccagca cattgtctcc cacacgcctc ctgaccttgt tccccgagcc 540
accatcctca gactcatcac tgagattgcc cgcactgtcg gctccactgg tatggctgca 600
ggccagtacg tcgaccttga aggaggtccc tttcctcttt cctttgttca ggagaagaaa 660
ttcggagcca tgggtgaatg ctctgccgtg tgcggtggcc tattgggcgg tgccactgag 720
gatgagctcc agagtctccg aaggtacggg agagccgtcg ggatgctgta tcaggtggtc 780
gatgacatca ccgaggacaa gaagaagagc tatgatggtg gagcagagaa gggaatgatg 840
gaaatggcgg aagagctcaa ggagaaggcg aagaaggagc ttcaagtgtt tgacaacaag 900
tatggaggag gagacacact tgttcctctc tacaccttcg ttgactacgc tgctcatcga 960
cattttcttc ttcccctctg a 981

<210> 19
<211> 245
<212> DNA
<213> GLycine sp

<400> 19
gcaacatctg ggactgggtt tgtcttgggg agtggtagtg ctgttgatct ttcggcactt 60
tcttgcactt gcttgggtac catgatggtt gctgcatctg ctaactcttt gaatcaggtg 120
tttgagatca ataatgatgc taaaatgaag agaacaagtc gcaggccact accctcagga 180
cgcatcacaa tacctcatgc agttggctgg gcatcctctg ttggattagc tggtacggct 240
ctact 245

<210> 20
<211> 253
<212> DNA
<213> Glycine sp

<400> 20
attggctttc caagatcatt gggttttctt gttgcattca tgaccttcta ctccttgggt 60
ttggcattgt ccaaggatat acctgacgtt gaaggagata aagagcacgg cattgattct 120
tttgcagtac gtctaggtca gaaacgggca ttttggattt gcgtttcctt ttttgaaatg 180
gctttcggag ttggtatcct ggccggagca tcatgctcac acttttggac taaaattttc 240
acgggtatgg gaa 253

<210> 21
<211> 275
<212> DNA
<213> Glycine sp

<400> 21
tgatcttcta ctctctgggt atggcattgt ccaaggatat atctgacgtt aaaggagata 60
aagcatacgg catcgatact ttagcgatac gtttgggtca aaaatgggta ttttggattt 120
gcattatcct ttttgaaatg gcttttggag ttgccctctt ggcaggagca acatcttctt 180
acctttggat taaaattgtc acgggtctgg gacatgctat tcttgcttca attctcttgt 240
accaagccaa atctatatac ttgagcaaca aagtt 275

<210> 22
<211> 299
<212> DNA
<213> Glycine sp

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

<400> 22
ccanaatang tncatcttng aaagacaatt ggcctcttca acacacaagt ctgcatgtga 60
agaagaggcc aattgtcttt ccaagatcac ttatngtggc tattgtaatc atgaacttct 120
tctttgtggg tatggcattg gcaaaggata tacctanctg ttgaaggaga taaaatatat 180
ggcattgata cttttgcaat acgtataggt caaaaacaag tattttggat ttgtattttc 240
ctttttgaaa ggctttcgga gtttccctag tggcaggagc aacatcttct agccttggt 299

<210> 23
<211> 767
<212> DNA
<213> Glycine sp

<400> 23
gtggaggctg tggttgctgc cctgtttatg aatatttata ttgttggttt gaatcaattg 60
tctgatgttg aaatagacaa gataaacaag ccgtatcttc cattagcatc tggggaatat 120
tcctttgaaa ctggtgtcac tattgttgca tctttttcaa ttctgagttt ttggcttggc 180
tgggttgtag gttcatggcc attattttgg gccctttttg taagctttgt gctaggaact 240
gcttattcaa tcaatgtgcc tctgttgaga tggaagaggt ttgcagtgct tgcagcgatg 300
tgcattctag ctgttcgggc agtaatagtt caacttgcat ttttccttca catgcagact 360
catgtgtaca agaggccacc tgtcttttca agaccattga tttttgctac tgcattcatg 420
agcttcttct ctgtagttat agcactgttt aaggatatac ctgacattga aggagataaa 480
gtatttggca tccaatcttt ttcagtgtgt ttaggtcaga agccggtgtt ctggacttgt 540
gttacccttc ttgaaatagc ttatggagtc gccctcctgg tgggagctgc atctccttgt 600
ctttggagca aaattttcac gggtctggga cacgctgtgc tggcttcaat tctctggttt 660
catgccaaat ctgtagattt gaaaagcaaa gcttcgataa catccttcta tatgtttatt 720
tggaagctat tttatgcaga atacttactc attccttttg ttagatg 767

<210> 24
<211> 255
<212> PRT
<213> Glycine sp

<400> 24
Val Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly
 1   5   10   15
Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr
            20   25   30
Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile
        35   40   45
Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly
    50   55   60
Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr
65   70   75   80
Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val
                85   90   95
Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu
            100   105   110
Ala Phe Phe Leu His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val

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Phe Ser Arg Pro Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser
    130                 135                 140
Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys
145                 150                 155                 160
Val Phe Gly Ile Gln Ser Phe Ser Val Cys Leu Gly Gln Lys Pro Val
                165                 170                 175
Phe Trp Thr Cys Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu
            180                 185                 190
Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly
        195                 200                 205
Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser
    210                 215                 220
Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile
225                 230                 235                 240
Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
                245                 250                 255
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<210> 25
<211> 360
<212> DNA
<213> Zea sp

<220>
<221> misc_feature
<222> (1)...(360)
<223> n = A,T,C or G

<400> 25
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tcaggcttat cttggcctga cattcaactg gggagcttta ctagggtggg ctgctattaa 120
ggaaagcata gaccctgcaa atcatccttc cattgtatac agctggtatt tgttggacgc 180
tggtgtatga tactatatat gcgcatcagg tgtttcgcta tccctacttt catattaatc 240
cttgatgaag tggccatttc atgttgtcgc ggtggtctta tacttgcata tctccatgca 300
tctcaggaca aagangatga cctgaaagta ggagtccaag tccacagctt aagatttggg 360

<210> 26
<211> 299
<212> DNA
<213> Zea sp

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

<400> 26
gatggttgca gcatctgcaa ataccctcaa ccaggtgttt gngataaaaa atgatgctaa 60
aatgaaaagg acaatgcgtg ccccctgcca tctggtcgca ttagtcctgc acatgctgcg 120
atgtgggcta caagtgttgg agttgcagga acagctttgt tggcctggaa ggctaatggc 180
ttggcagctg ggcttgcagc ttctaatctt gttctgtatg catttgtgta tacgccgttg 240
aagcaaatac accctgttaa tacatgggtt ggggcagtcg ttggtgccat cccaccact 299

<210> 27
<211> 255
<212> DNA
<213> Zea sp

<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A,T,C or G

<400> 27
anacttgcat atctccatgc ntctcaggac aaagangatg acctgaaagt aggtgtcaag 60
tccacagcat taagatttgg agatttgacc nnatactgna tcagtggctt tggcgcggca 120
tgcttcggca gcttagcact cagtggttac aatgctgacc ttggttggtg tttagtgtga 180

tgcttgagcg aagaatggta tngtttttac ttgatattga ctccagacct gaaatcatgt 240
tggacagggt ggccc 255

<210> 28
<211> 257
<212> DNA
<213> Zea sp

<400> 28
attgaagggg ataggactct ggggcttcag tcacttcctg ttgcttttgg gatggaaact 60
gcaaaatgga tttgtgttgg agcaattgat atcactcaat tatctgttgc aggttaccta 120
ttgagcaccg gtaagctgta ttatgccctg gtgttgcttg ggctaacaat tcctcaggtg 180
ttctttcagt tccagtactt cctgaaggac cctgtgaagt atgatgtcaa atatcaggca 240
agcgcacaac cattctt 257

<210> 29
<211> 368
<212> DNA
<213> Zea sp

<400> 29
atccagttgc aaataataat ggcgttcttc tctgttgtaa tagcactatt caaggatata 60
cctgacatcg aaggggaccg catattcggg atccgatcct tcagcgtccg gttagggcaa 120
aagaaggtct tttggatctg cgttggcttg cttgagatgg cctacagcgt tgcgatactg 180
atgggagcta cctcttcctg tttgtggagc aaaacagcaa ccatcgctgg ccattccata 240
cttgccgcga tcctatggag ctgcgcgcga tcggtggact tgacgagcaa agccgcaata 300
acgtccttct acatgttcat ctggaagctg ttctacgcgg agtacctgct catccctctg 360
gtgcggtg 368

<210> 30
<211> 122
<212> PRT
<213> Zea sp

<400> 30
Ile Gln Leu Gln Ile Ile Met Ala Phe Phe Ser Val Val Ile Ala Leu
1 5 10 15
Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg
20 25 30
Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val Phe Trp Ile Cys Val
35 40 45
Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile Leu Met Gly Ala Thr
50 55 60
Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile Ala Gly His Ser Ile
65 70 75 80
Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg Ser Val Asp Leu Thr Ser
85 90 95
Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr
100 105 110
Ala Glu Tyr Leu Leu Ile Pro Leu Val Arg
115 120

<210> 31
<211> 278
<212> DNA
<213> Zea sp

<400> 31
tattcagcac cacctctcaa gctcaagcag aatggatgga ttgggaactt cgctctgggt 60
gcgagttaca tcagcttgcc ctggtgggct ggccaggcgt tatttggaac tcttacacca 120
gatatcattg tcttgactac tttgtacagc atagctgggc tagggattgc tattgtaaat 180
gatttcaaga gtattgaagg ggataggact ctggggcttc agtcacttcc tgttgctttt 240
gggatggaaa ctgcaaaatg gatttgtgtt ggagcaat 278

<210> 32
<211> 292

<212> PRT
<213> Synechocystis sp

<400> 32
Met Val Ala Gln Thr Pro Ser Ser Pro Pro Leu Trp Leu Thr Ile Ile
 1   5   10   15
Tyr Leu Leu Arg Trp His Lys Pro Ala Gly Arg Leu Ile Leu Met Ile
            20   25   30
Pro Ala Leu Trp Ala Val Cys Leu Ala Ala Gln Gly Leu Pro Pro Leu
        35   40   45
Pro Leu Leu Gly Thr Ile Ala Leu Gly Thr Leu Ala Thr Ser Gly Leu
    50   55   60
Gly Cys Val Val Asn Asp Leu Trp Asp Arg Asp Ile Asp Pro Gln Val
65   70   75   80
Glu Arg Thr Lys Gln Arg Pro Leu Ala Ala Arg Ala Leu Ser Val Gln
                85   90   95
Val Gly Ile Gly Val Ala Leu Val Ala Leu Leu Cys Ala Ala Gly Leu
            100   105   110
Ala Phe Tyr Leu Thr Pro Leu Ser Phe Trp Leu Cys Val Ala Ala Val
        115   120   125
Pro Val Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro
    130   135   140
Gln Leu Val Leu Ser Ile Ala Trp Gly Phe Ala Val Leu Ile Ser Trp
145   150   155   160
Ser Ala Val Thr Gly Asp Leu Thr Asp Ala Thr Trp Val Leu Trp Gly
                165   170   175
Ala Thr Val Phe Trp Thr Leu Gly Phe Asp Thr Val Tyr Ala Met Ala
            180   185   190
Asp Arg Glu Asp Asp Arg Arg Ile Gly Val Asn Ser Ser Ala Leu Phe
        195   200   205
Phe Gly Gln Tyr Val Gly Glu Ala Val Gly Ile Phe Phe Ala Leu Thr
    210   215   220
Ile Gly Cys Leu Phe Tyr Leu Gly Met Ile Leu Met Leu Asn Pro Leu
225   230   235   240
Tyr Trp Leu Ser Leu Ala Ile Ala Ile Val Gly Trp Val Ile Gln Tyr
                245   250   255
Ile Gln Leu Ser Ala Pro Thr Pro Glu Pro Lys Leu Tyr Gly Gln Ile
            260   265   270
Phe Gly Gln Asn Val Ile Ile Gly Phe Val Leu Leu Ala Gly Met Leu
        275   280   285
Leu Gly Trp Leu
    290

<210> 33
<211> 316
<212> PRT
<213> Synechocystis sp

<400> 33
Met Val Thr Ser Thr Lys Ile His Arg Gln His Asp Ser Met Gly Ala
 1   5   10   15
Val Cys Lys Ser Tyr Tyr Gln Leu Thr Lys Pro Arg Ile Ile Pro Leu
            20   25   30
Leu Leu Ile Thr Thr Ala Ala Ser Met Trp Ile Ala Ser Glu Gly Arg
        35   40   45
Val Asp Leu Pro Lys Leu Leu Ile Thr Leu Leu Gly Gly Thr Leu Ala
    50   55   60
Ala Ala Ser Ala Gln Thr Leu Asn Cys Ile Tyr Asp Gln Asp Ile Asp
65   70   75   80
Tyr Glu Met Leu Arg Thr Arg Ala Arg Pro Ile Pro Ala Gly Lys Val
                85   90   95
Gln Pro Arg His Ala Leu Ile Phe Ala Leu Ala Leu Gly Val Leu Ser
            100   105   110
Phe Ala Leu Leu Ala Thr Phe Val Asn Val Leu Ser Gly Cys Leu Ala
        115   120   125

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Leu Ser Gly Ile Val Phe Tyr Met Leu Val Tyr Thr His Trp Leu Lys
    130                 135                 140
Arg His Thr Ala Gln Asn Ile Val Ile Gly Gly Ala Ala Gly Ser Ile
145                 150                 155                 160
Pro Pro Leu Val Gly Trp Ala Ala Val Thr Gly Asp Leu Ser Trp Thr
                165                 170                 175
Pro Trp Val Leu Phe Ala Leu Ile Phe Leu Trp Thr Pro Pro His Phe
            180                 185                 190
Trp Ala Leu Ala Leu Met Ile Lys Asp Asp Tyr Ala Gln Val Asn Val
        195                 200                 205
Pro Met Leu Pro Val Ile Ala Gly Glu Glu Lys Thr Val Ser Gln Ile
    210                 215                 220
Trp Tyr Tyr Ser Leu Leu Val Val Pro Phe Ser Leu Leu Leu Val Tyr
225                 230                 235                 240
Pro Leu His Gln Leu Gly Ile Leu Tyr Leu Ala Ile Ala Ile Ile Leu
                245                 250                 255
Gly Gly Gln Phe Leu Val Lys Ala Trp Gln Leu Lys Gln Ala Pro Gly
            260                 265                 270
Asp Arg Asp Leu Ala Arg Gly Leu Phe Lys Phe Ser Ile Phe Tyr Leu
        275                 280                 285
Met Leu Leu Cys Leu Ala Met Val Ile Asp Ser Leu Pro Val Thr His
    290                 295                 300
Gln Leu Val Ala Gln Met Gly Thr Leu Leu Leu Gly
305                 310                 315
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<210> 34
<211> 324
<212> PRT
<213> Synechocystis sp

<400> 34

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Met Ser Asp Thr Gln Asn Thr Gly Gln Asn Gln Ala Lys Ala Arg Gln
 1                5                  10                  15
Leu Leu Gly Met Lys Gly Ala Ala Pro Gly Glu Ser Ser Ile Trp Lys
            20                  25                  30
Ile Arg Leu Gln Leu Met Lys Pro Ile Thr Trp Ile Pro Leu Ile Trp
        35                  40                  45
Gly Val Val Cys Gly Ala Ala Ser Ser Gly Gly Tyr Ile Trp Ser Val
    50                  55                  60
Glu Asp Phe Leu Lys Ala Leu Thr Cys Met Leu Leu Ser Gly Pro Leu
65                  70                  75                  80
Met Thr Gly Tyr Thr Gln Thr Leu Asn Asp Phe Tyr Asp Arg Asp Ile
                85                  90                  95
Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala Ile Ser
            100                 105                 110
Val Pro Gln Val Val Thr Gln Ile Leu Ile Leu Leu Val Ala Gly Ile
        115                 120                 125
Gly Val Ala Tyr Gly Leu Asp Val Trp Ala Gln His Asp Phe Pro Ile
    130                 135                 140
Met Met Val Leu Thr Leu Gly Gly Ala Phe Val Ala Tyr Ile Tyr Ser
145                 150                 155                 160
Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Leu Gly Asn Tyr Ala
                165                 170                 175
Leu Gly Ala Ser Tyr Ile Ala Leu Pro Trp Trp Ala Gly His Ala Leu
            180                 185                 190
Phe Gly Thr Leu Asn Pro Thr Ile Met Val Leu Thr Leu Ile Tyr Ser
        195                 200                 205
Leu Ala Gly Leu Gly Ile Ala Val Val Asn Asp Phe Lys Ser Val Glu
    210                 215                 220
Gly Asp Arg Gln Leu Gly Leu Lys Ser Leu Pro Val Met Phe Gly Ile
225                 230                 235                 240
Gly Thr Ala Ala Trp Ile Cys Val Ile Met Ile Asp Val Phe Gln Ala
                245                 250                 255
Gly Ile Ala Gly Tyr Leu Ile Tyr Val His Gln Gln Leu Tyr Ala Thr
            260                 265                 270
```

```
Ile Val Leu Leu Leu Leu Ile Pro Gln Ile Thr Phe Gln Asp Met Tyr
        275                 280                 285
Phe Leu Arg Asn Pro Leu Glu Asn Asp Val Lys Tyr Gln Ala Ser Ala
    290                 295                 300
Gln Pro Phe Leu Val Phe Gly Met Leu Ala Thr Gly Leu Ala Leu Gly
305                 310                 315                 320
His Ala Gly Ile
```

<210> 35
<211> 307
<212> PRT
<213> Synechocystis sp

<400> 35

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Met Thr Glu Ser Ser Pro Leu Ala Pro Ser Thr Ala Pro Ala Thr Arg
 1               5                  10                  15
Lys Leu Trp Leu Ala Ala Ile Lys Pro Pro Met Tyr Thr Val Ala Val
            20                  25                  30
Val Pro Ile Thr Val Gly Ser Ala Val Ala Tyr Gly Leu Thr Gly Gln
        35                  40                  45
Trp His Gly Asp Val Phe Thr Ile Phe Leu Leu Ser Ala Ile Ala Ile
    50                  55                  60
Ile Ala Trp Ile Asn Leu Ser Asn Asp Val Phe Asp Ser Asp Thr Gly
65                  70                  75                  80
Ile Asp Val Arg Lys Ala His Ser Val Val Asn Leu Thr Gly Asn Arg
                85                  90                  95
Asn Leu Val Phe Leu Ile Ser Asn Phe Phe Leu Leu Ala Gly Val Leu
            100                 105                 110
Gly Leu Met Ser Met Ser Trp Arg Ala Gln Asp Trp Thr Val Leu Glu
        115                 120                 125
Leu Ile Gly Val Ala Ile Phe Leu Gly Tyr Thr Tyr Gln Gly Pro Pro
    130                 135                 140
Phe Arg Leu Gly Tyr Leu Gly Leu Gly Glu Leu Ile Cys Leu Ile Thr
145                 150                 155                 160
Phe Gly Pro Leu Ala Ile Ala Ala Ala Tyr Tyr Ser Gln Ser Gln Ser
                165                 170                 175
Phe Ser Trp Asn Leu Leu Thr Pro Ser Val Phe Val Gly Ile Ser Thr
            180                 185                 190
Ala Ile Ile Leu Phe Cys Ser His Phe His Gln Val Glu Asp Asp Leu
        195                 200                 205
Ala Ala Gly Lys Lys Ser Pro Ile Val Arg Leu Gly Thr Lys Leu Gly
    210                 215                 220
Ser Gln Val Leu Thr Leu Ser Val Val Ser Leu Tyr Leu Ile Thr Ala
225                 230                 235                 240
Ile Gly Val Leu Cys His Gln Ala Pro Trp Gln Thr Leu Leu Ile Ile
                245                 250                 255
Ala Ser Leu Pro Trp Ala Val Gln Leu Ile Arg His Val Gly Gln Tyr
            260                 265                 270
His Asp Gln Pro Glu Gln Val Ser Asn Cys Lys Phe Ile Ala Val Asn
        275                 280                 285
Leu His Phe Phe Ser Gly Met Leu Met Ala Ala Gly Tyr Gly Trp Ala
    290                 295                 300
Gly Leu Gly
305
```

<210> 36
<211> 927
<212> DNA
<213> Synechocystis sp

<400> 36

```
atggcaacta tccaagcttt ttggcgcttc tcccgccccc ataccatcat tggtacaact      60
ctgagcgtct gggctgtgta tctgttaact attctcgggg atggaaactc agttaactcc     120
cctgcttccc tggatttagt gttcggcgct tggctggcct gcctgttggg taatgtgtac     180
attgtcggcc tcaaccaatt gtgggatgtg gacattgacc gcatcaataa gccgaatttg     240
```

```
cccctagcta acggagattt ttctatcgcc cagggccgtt ggattgtggg actttgtggc     300
gttgcttcct tggcgatcgc ctggggatta gggctatggc tggggctaac ggtgggcatt     360
agtttgatta ttggcacggc ctattcggtg ccgccagtga ggttaaagcg cttttccctg     420
ctggcggccc tgtgtattct gacggtgcgg ggaattgtgg ttaacttggg cttatttta      480
ttttttagaa ttggtttagg ttatcccccc actttaataa ccccccatctg ggttttgact    540
ttatttatct tagttttcac cgtggcgatc gccatttta aagatgtgcc agatatggaa      600
ggcgatcggc aatttaagat tcaaacttta actttgcaaa tcggcaaaca aaacgttttt     660
cggggaacct taattttact cactggttgt tatttagcca tggcaatctg gggcttatgg     720
gcggctatgc ctttaaatac tgctttcttg attgtttccc atttgtgctt attagcctta     780
ctctggtggc ggagtcgaga tgtacactta gaaagcaaaa ccgaaattgc tagtttttat     840
cagtttattt ggaagctatt tttcttagag tacttgctgt atcccttggc tctgtggtta     900
cctaattttt ctaatactat tttttag                                        927
```

<210> 37
<211> 308
<212> PRT
<213> Synechocystis sp

<400> 37

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Met Ala Thr Ile Gln Ala Phe Trp Arg Phe Ser Arg Pro His Thr Ile
 1               5                  10                  15
Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
            20                  25                  30
Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
        35                  40                  45
Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
    50                  55                  60
Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65                  70                  75                  80
Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
                85                  90                  95
Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
            100                 105                 110
Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
        115                 120                 125
Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
    130                 135                 140
Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
145                 150                 155                 160
Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
                165                 170                 175
Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
            180                 185                 190
Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln
        195                 200                 205
Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
    210                 215                 220
Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
225                 230                 235                 240
Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
                245                 250                 255
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
            260                 265                 270
Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
        275                 280                 285
Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
    290                 295                 300
Asn Thr Ile Phe
305
```

<210> 38
<211> 1092
<212> DNA
<213> Synechocystis sp

<400> 38
atgaaatttc cgccccacag tggttaccat tggcaaggtc aatcaccttt ctttgaaggt 60
tggtacgtgc gcctgctttt gccccaatcc ggggaaagtt ttgcttttat gtactccatc 120
gaaaatcctg ctagcgatca tcattacggc ggcggtgctg tgcaaatttt agggccggct 180
acgaaaaaac aagaaaatca ggaagaccaa cttgtttggc ggacatttcc ctcggtaaaa 240
aaatttgggg ccagtcctcg ccagtttgcc ctagggcatt ggggaaaatg tagggataac 300
aggcaggcga aacccctact ctccgaagaa ttttttgcca cggtcaagga aggttatcaa 360
atccatcaaa atcagcacca aggacaaatc attcatggcg atcgccattg tcgttggcag 420
ttcaccgtag aaccggaagt aacttggggg agtcctaacc gatttcctcg ggctacagcg 480
ggttggcttt ccttttttacc cttgtttgat cccggttggc aaattctttt agcccaaggt 540
agagcgcacg gctggctgaa atggcagagg gaacagtatg aatttgacca cgccctagtt 600
tatgccgaaa aaaattgggg tcactccttt ccctcccgct ggttttggct ccaagcaaat 660
tattttcctg accatccagg actgagcgtc actgccgctg gcggggaacg gattgttctt 720
ggtcgccccg aagaggtagc tttaattggc ttacatcacc aaggtaattt ttacgaattt 780
ggcccgggcc atggcacagt cacttggcaa gtagctccct ggggccgttg gcaattaaaa 840
gccagcaatg ataggtattg ggtcaagttg tccggaaaaa cagataaaaa aggcagttta 900
gtccacactc ccaccgccca gggcttacaa ctcaactgcc gagataccac taggggctat 960
ttgtatttgc aattgggatc tgtgggtcac ggcctgatag tgcaagggga aacggacacc 1020
gcggggctag aagttggagg tgattggggt ttaacagagg aaaatttgag caaaaaaaca 1080
gtgccattct ga 1092

<210> 39
<211> 363
<212> PRT
<213> Synechocystis sp

<400> 39
Met Lys Phe Pro Pro His Ser Gly Tyr His Trp Gln Gly Gln Ser Pro
 1   5   10   15
Phe Phe Glu Gly Trp Tyr Val Arg Leu Leu Leu Pro Gln Ser Gly Glu
            20   25   30
Ser Phe Ala Phe Met Tyr Ser Ile Glu Asn Pro Ala Ser Asp His His
        35   40   45
Tyr Gly Gly Gly Ala Val Gln Ile Leu Gly Pro Ala Thr Lys Lys Gln
    50   55   60
Glu Asn Gln Glu Asp Gln Leu Val Trp Arg Thr Phe Pro Ser Val Lys
65   70   75   80
Lys Phe Trp Ala Ser Pro Arg Gln Phe Ala Leu Gly His Trp Gly Lys
                85   90   95
Cys Arg Asp Asn Arg Gln Ala Lys Pro Leu Leu Ser Glu Glu Phe Phe
            100   105   110
Ala Thr Val Lys Glu Gly Tyr Gln Ile His Gln Asn Gln His Gln Gly
        115   120   125
Gln Ile Ile His Gly Asp Arg His Cys Arg Trp Gln Phe Thr Val Glu
    130   135   140
Pro Glu Val Thr Trp Gly Ser Pro Asn Arg Phe Pro Arg Ala Thr Ala
145   150   155   160
Gly Trp Leu Ser Phe Leu Pro Leu Phe Asp Pro Gly Trp Gln Ile Leu
                165   170   175
Leu Ala Gln Gly Arg Ala His Gly Trp Leu Lys Trp Gln Arg Glu Gln
            180   185   190
Tyr Glu Phe Asp His Ala Leu Val Tyr Ala Glu Lys Asn Trp Gly His
        195   200   205
Ser Phe Pro Ser Arg Trp Phe Trp Leu Gln Ala Asn Tyr Phe Pro Asp
    210   215   220
His Pro Gly Leu Ser Val Thr Ala Ala Gly Gly Glu Arg Ile Val Leu
225   230   235   240
Gly Arg Pro Glu Glu Val Ala Leu Ile Gly Leu His His Gln Gly Asn
                245   250   255
Phe Tyr Glu Phe Gly Pro Gly His Gly Thr Val Thr Trp Gln Val Ala
            260   265   270
Pro Trp Gly Arg Trp Gln Leu Lys Ala Ser Asn Asp Arg Tyr Trp Val
        275   280   285
Lys Leu Ser Gly Lys Thr Asp Lys Lys Gly Ser Leu Val His Thr Pro
    290   295   300

Thr Ala Gln Gly Leu Gln Leu Asn Cys Arg Asp Thr Thr Arg Gly Tyr
305 310 315 320
Leu Tyr Leu Gln Leu Gly Ser Val Gly His Gly Leu Ile Val Gln Gly
325 330 335
Glu Thr Asp Thr Ala Gly Leu Glu Val Gly Gly Asp Trp Gly Leu Thr
340 345 350
Glu Glu Asn Leu Ser Lys Lys Thr Val Pro Phe
355 360

<210> 40
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 40
cgcgatttaa atggcgcgcc ctgcaggcgg ccgcctgcag ggcgcgccat ttaaat 56

<210> 41
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 41
tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 42
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 42
tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 43
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 43
tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 44
tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 45
<211> 36

212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 45
tcgaggatcc gcggccgcaa gcttcctgca ggagct 36

<210> 46
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 46
cctgcaggaa gcttgcggcc gcggatcc 28

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 47
tcgacctgca ggaagcttgc ggccgcggat ccagct 36

<210> 48
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 48
ggatccgcgg ccgcaagctt cctgcagg 28

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 49
gatcacctgc aggaagcttg cggccgcgga tccaatgca 39

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 50
ttggatccgc ggccgcaagc ttcctgcagg t 31

<210> 51
<211> 41

212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 51
ggatccgcgg ccgcacaatg gagtctctgc tctctagttc t 41

<210> 52
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 52
ggatcctgca ggtcacttca aaaaaggtaa cagcaagt 38

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 53
ggatccgcgg ccgcacaatg gcgtttttg ggctctcccg tgttt 45

<210> 54
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 54
ggatcctgca ggttattgaa aacttcttcc aagtacaact 40

<210> 55
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 55
ggatccgcgg ccgcacaatg tggcgaagat ctgttgtt 38

<210> 56
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 56
ggatcctgca ggtcatggag agtagaagga aggagct 37

<210> 57
<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 57
ggatccgcgg ccgcacaatg gtacttgccg aggttccaaa gcttgcctct 50

<210> 58
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 58
ggatcctgca ggtcacttgt ttctggtgat gactctat 38

<210> 59
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 59
ggatccgcgg ccgcacaatg acttcgattc tcaacact 38

<210> 60
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 60
ggatcctgca ggtcagtgtt gcgatgctaa tgccgt 36

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 61
taatgtgtac attgtcggcc tc 22

<210> 62
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 62
gcaatgtaac atcagagatt ttgagacaca acgtggcttt ccacaattcc ccgcaccgtc 60

<210> 63
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 63
aggctaataa gcacaaatgg ga 22

<210> 64
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 64
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggaattgg tttaggttat 60
ccc 63

<210> 65
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 65
ggatccatgg ttgcccaaac cccatc 26

<210> 66
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 66
gcaatgtaac atcagagatt ttgagacaca acgtggcttt gggtaagcaa caatgaccgg 60
c 61

<210> 67
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 67
gaattctcaa agccagccca gtaac 25

<210> 68
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 68
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgggtgcga aaagggtttt 60
ccc 63

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 69
ccagtggttt aggctgtgtg gtc 23

<210> 70
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 70
ctgagttgga tgtattggat c 21

<210> 71
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 71
ggatccatgg ttacttcgac aaaaatcc 28

<210> 72
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 72
gcaatgtaac atcagagatt ttgagacaca acgtggcttt gctaggcaac cgcttagtac 60

<210> 73
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 73
gaattcttaa cccaacagta aagttccc 28

<210> 74
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 74
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgccggcat tgtcttttac 60
atg 63

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 75
ggaacccttg cagccgcttc 20

<210> 76
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 76
gtatgcccaa ctggtgcaga gg 22

<210> 77
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 77
ggatccatgt ctgacacaca aaataccg 28

<210> 78
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 78
gcaatgtaac atcagagatt ttgagacaca acgtggcttt cgccaatacc agccaccaac 60
ag 62

<210> 79
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 79
gaattctcaa atccccgcat ggcctag 27

<210> 80
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 80
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggcctacg gcttggacgt 60
gtggg 65

<210> 81
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 81
cacttggatt cccctgatct g 21

<210> 82
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 82
gcaatacccg cttggaaaac g 21

<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 83
ggatccatga ccgaatcttc gcccctagc 29

<210> 84
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 84
gcaatgtaac atcagagatt ttgagacaca acgtggcttt caatcctagg tagccgaggc 60
g 61

<210> 85
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 85
gaattcttag cccaggccag cccagcc 27

<210> 86
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 86
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggggaatt gatttgttta 60
attacc 66

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 87
gcgatcgcca ttatcgcttg g 21

<210> 88
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 88
gcagactggc aattatcagt aacg 24

<210> 89
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 89
ccatggattc gagtaaagtt gtcgc 25

<210> 90
<211> 25
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 90
gaattcactt caaaaaaggt aacag 25

<210> 91
<211> 4550
<212> DNA
<213> Arabidopsis sp

<400> 91
attttacacc aatttgatca cttaactaaa ttaattaaat tagatgatta tcccaccata 60
tttttgagca ttaaaccata aaaccatagt tataagtaac tgttttaatc gaatatgact 120
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